

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 16, 2003, 16:37:55 : Search time 1441.15 Seconds
(without alignments)
15778.007 Million cell updates/sec

Title: US-09-497-967-3
Perfect score: 1404
Sequence: 1 atgaaataataatttagt.....tgattttattattatta 1404

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST: *
1: em_estba: *
2: em_estchum: *
3: em_estin: *
4: em_estmu: *
5: em_estov: *
6: em_estpl: *
7: em_estro: *
8: em_estc: *
9: gb_estli: *
10: gb_est2: *
11: gb_hic: *
12: gb_est3: *
13: gb_est4: *
14: gb_est5: *
15: em_estfun: *
16: em_estom: *
17: gb_gss: *
18: em_gss_hum: *
19: em_gss_inv: *
20: em_gss_pln: *
21: em_gss_vrt: *
22: em_gss_fun: *
23: em_gss_mam: *
24: em_gss_mus: *
25: em_gss_other: *
26: em_gss_pro: *
27: em_gss_rod: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	204.2	14.5	658	14	BQ135057
C 2	199.8	14.2	607	14	BQ134912
C 3	192.6	13.7	602	14	BQ135164
C 4	191.6	13.6	590	14	BQ135179
C 5	165.6	11.8	502	14	BQ134889
C 6	159.4	11.4	445	14	BQ134871

C 7	151.4	10.8	419	14	BQ135036
C 8	134.4	9.6	675	14	BQ135196
C 9	127.8	9.1	599	14	BQ134821
C 10	115.2	8.2	540	14	BQ134879
C 11	113.8	8.1	538	14	BQ134810
C 12	110.4	7.9	630	14	BQ134905
C 13	110.4	7.9	631	14	BQ134827
C 14	109.4	7.8	523	14	BQ134970
C 15	106.4	7.6	514	14	BQ134761
C 16	106.4	7.6	661	14	BQ135189
C 17	105.8	7.5	560	14	BQ135129
C 18	105.8	7.5	622	14	BQ134798
C 19	103.2	7.4	687	14	BQ135168
C 20	103.2	7.4	337	14	BQ134748
C 21	99.2	7.1	592	14	BQ134985
C 22	72.2	5.1	210	14	BQ134900
C 23	69.8	5.0	150	14	BQ135114
C 24	68.4	4.9	773	17	CNS01VTG
C 25	62	4.4	735	17	CNS04NSM
C 26	61.4	4.4	470	17	FR0018463
C 27	61.4	4.4	989	17	CNS02HA4
C 28	61.2	4.4	1101	17	CNS0039C
C 29	60.8	4.3	501	17	FR0048173
C 30	58.4	4.2	605	17	AZ640388
C 31	57.8	4.1	813	13	BJ406459
C 32	56.2	4.0	494	17	FR0048073
C 33	56.2	4.0	572	17	CNS043SN
C 34	56.2	4.0	723	17	BH182027
C 35	56.2	4.0	723	17	CNS07NIN
C 36	56	4.0	824	17	AZ185454
C 37	56	4.0	898	17	CNS04ALV
C 38	55.6	4.0	450	17	FR0025683
C 39	55.4	3.9	623	9	AU060774
C 40	55.4	3.9	742	9	AU060168
C 41	55	3.9	619	17	FR0006944
C 42	55	3.9	805	17	CNS04RW2
C 43	55	3.9	857	13	BJ403229
C 44	55	3.9	1101	17	CNS0039G
C 45	54.8	3.9	550	17	FR0043207

ALIGNMENTS

RESULT 1
BQ135057/c

LOCUS
INIT1.2.G01.g1.A006 G5 trophont cDNA (INIT1) Ichthyophthirius

DEFINITION
multifiliis cDNA, mRNA sequence.

ACCESSION
BQ135057

VERSION
BQ135057.1

KEYWORDS
EST.

SOURCE
Ichthyophthirius multifiliis

ORGANISM
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;

REFERENCE
1 (bases 1 to 658)

AUTHORS
Clark, T., Cordonnier-Pratt, M.-M., Sudman, M., Wentzel, V., Gingle, A.,

TITLE
Dickerson, H., Lin, T.-L. and Pratt, L.H.

JOURNAL
An EST database for Ichthyophthirius multifiliis (G5 isolate)

COMMENT
Unpublished (2002)

Contact: Cordonnier-Pratt MM

Laboratory for Genomics and Bioinformatics

The University of Georgia, Department of Plant Biology

Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA

Tel: 706 542 1860

Fax: 706 583 0210

Email: mmpratt@uga.edu

Sequences have been trimmed to exclude PolyA, vector, and regions

below Phred quality 16. The threshold for highest quality sequence

is 20.

Seq primer: T7

High quality sequence start: 67

BQ135057 658 bp mRNA linear EST 22-APR-2002
INIT1.2.G01.g1.A006 G5 trophont cDNA (INIT1) Ichthyophthirius
multifiliis cDNA, mRNA sequence.

BQ135057.1 GI:20261156
EST.

Ichthyophthirius multifiliis.
Ichthyophthirius multifiliis

Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Ophryoglenina; Ichthyophthirius.

1 (bases 1 to 658)
Clark, T., Cordonnier-Pratt, M.-M., Sudman, M., Wentzel, V., Gingle, A.,

Dickerson, H., Lin, T.-L. and Pratt, L.H.
An EST database for Ichthyophthirius multifiliis (G5 isolate)

Unpublished (2002)

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Tel: 706 542 1860

Fax: 706 583 0210

Email: mmpratt@uga.edu

Sequences have been trimmed to exclude PolyA, vector, and regions

below Phred quality 16. The threshold for highest quality sequence

is 20.

Seq primer: T7

BQ135036 INIT1.2_D
BQ135196 INIT1.4_E
BQ134821 INIT1.4_D
BQ134879 INIT1.1_C
BQ134810 INIT1.1_C
BQ134905 INIT1.1_F
BQ134827 INIT1.4_E
BQ134970 INIT1.2_D
BQ134761 INIT1.3_F
BQ135189 INIT1.4_D
BQ135129 INIT1.3_F
BQ134798 INIT1.4_B
BQ135168 INIT1.4_B
BQ134748 INIT1.3_E
BQ134985 INIT1.2_G
BQ134900 INIT1.1_E
BQ135114 INIT1.3_E
AL169549 Tetraodon
AL299119 Tetraodon
AL011359 F.rubripe
AL137365 Tetraodon
AL063921 Drosophil
AL444958 Fugu rubr
AZ640388 IM0502E21
BJ406459 BJ406459
AL444858 Fugu rubr
AL273200 Tetraodon
BH182027 020_K_19-
AL618977 T3 end of
AZ185454 SP_1005_A
AL282028 Tetraodon
AL018519 F.rubripe
AU060774 AU060774
AU060168 AU060168
Z90754 F.rubripes
AL304427 Tetraodon
BJ403229 BJ403229
AL063921 Drosophil
AL130699 Fugu rubr

Thu Feb 20 11:10:20 2003

Eukaryota: Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Ophryoglenina; Ichthyophthirius.	
REFERENCE	1. (bases 1 to 607)
AUTHORS	Clark,T., Cordonnier-Pratt,M.-M., Sudman,M., Wentzel,V., Gingle,A., Dickerson,H., Lin,T.-L. and Pratt,L.H.
TITLE	An EST database for Ichthyophthirius multifiliis (G5 isolate)
JOURNAL	Unpublished (2002)
COMMENT	Contact: Cordonnier-Pratt MM Laboratory for Genomics and Bioinformatics The University of Georgia, Department of Plant Biology Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA Tel: 706 542 1860 Fax: 706 583 0210 Email: mmpratt@uga.edu Sequences have been trimmed to exclude polyA, vector, and regions below Phred quality 16. The threshold for highest quality sequence is 20. Seq primer: JEN REV High quality sequence stop: 599 POLYA=No.
FEATURES	Location/Qualifiers
source	1..607 /organism="Ichthyophthirius multifiliis" /strain="G5" /db_xref="taxon:5932" /note="Vector: pBluescript SK(-) from Lambda Zap II; Site.1: EcoRI; Site.2: EcoRI; The library was made from trophont polyA+ RNA of the G5 parasite strain. Double-stranded cDNA was linked to EcoRI adaptors, size fractionated, and material >500 bp cloned into lambda ZAP II. Plasmid DNA for sequencing was prepared by mass excision."
BASE COUNT	199 a 111 c 104 g 193 t
ORIGIN	
Query Match	14.2%; Score 199.8; DB 14; Length 607;
Best Local Similarity	65.6%; Pred. No. 2.8e-33;
Matches 377; Conservative	0; Mismatches 177; Indels 21; Gaps 5;
QY	841 AGTACATGCCCTACCTGCCAGCAATAAAGATTATGGTCTCGAAGCCACTGCAGGTGGT 900
DB	607 AGTAATGCGTAGTTCGGAATCAAAAAGACCAA---TTCCTTAATCCAGATCAGGTCTT 551
QY	901 GCCGCTACTTTAGCCAAATATGTAATTTGCATGCGCTGATGCTACTGCAATTTGCTAGT 960
DB	550 GAGGCTAATTTAGCCGATATATGTCGCACTGAATGCTCTGCTGGCACTCTGTTTACAGAC 491
QY	961 GGAGCAA---CTAATTTGTAATATTATAACAGAAATGCTAAATTTGCTGCTAACTTT 1017
DB	490 GGAGTAACACCTACTTACTGTATCATCTCTAATAATGTTAATTTGAAGCTGGCTTT 431
QY	1018 TATTTTGATGGTAATAATTTCTAGGCAGGAAGTAGTAGATGCAAGCATGTCAGCAAA 1077
DB	430 TACT---AAAATAGTAATTTTCAAGCAGGTAAAAGTTAATGCAATAAGTGTGCAAGTAAGT 374
QY	1078 AAAGTTTAAAGCGCTGTAGCAACTGCAGGTGGTACTGCTACTTTAATTCATATGTGCC 1137
DB	373 AAAACT---GGTTCAGCATCTGTTCCAGGTAAATAGTGTACTTCCAGCCACATATGTTAA 317
QY	1138 CTTGAATGCCCTGCTGGTACTGTACTACCGATGGAACAACATCTACTTATAAATAAGCA 1197
DB	316 AACGATTGCGCTGCTGGTACAGTGGTTGATGGTACATCACTAATTTTGTAGCTTTA 257
QY	1198 GCATCTGAATGTGTTAAATGTCTGCCAACTTTTATACTACAAAATAAATGATGGGTA 1257
DB	256 GCAAGTGAATGTAATAATGTTAGGCTAACTTTTATGATCAAAAACATCTCTGGTTTTGCA 197
QY	1258 GCAGGTATTGATACATGTACTAGTTGTAATAAATAAATTAACCTTCTGGCGCTGAAGCTAAT 1317
DB	196 GCAGGTACTGATACATGTACTGAATGTTCTTAAAAAATTAACCTTCTGGTGTCTACACGCTAAA 137
QY	1318 TTACCTGAATCTGCTAAAAAATAATATATGTC-----ATTTGCTGAATTTT 1368

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QY 894 AGGTGGTGGCGCTACTTTAGCCAAATAATGTAATATGCGATGCCGTGAGTACTCAAT 953
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Db 590 AGGCTTGAGGCTAATTTAGCGCATAATGCGCACTGGAATGCTGCTGCCACTTGT 531
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 954 TCGTAGTGAGCAA---CTAATTATGTAATATTATAACAGAGTCTAAATTTGCTGC 1010
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Db 530 TACAGACGAGTACACCTACTTACTGATGATCACTCTCATATGTTGTAATGTAAGC 471
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1011 TAACCTTTTATTTGATGTAATAATTTCTAGCGAGAGTAGTAGTCAAGCATGTCC 1070
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Db 470 TGGCTTTTACTAAA---TAGTAATTTGAGAGCAGGTAAAGTAAATGCAATAAGTGTG 414
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QY 1071 AGCAATAAAGTTTAAGCGGTGTAGCAACTGCGAGGTGTACTGCTACTTTAATTCGATA 1130
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Db 413 AGTAAGTAAACT---GGTTGAGCATCTGTTCCAGGTAATAGTCTACTTTCCAGCCACATA 357
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1131 ATGTGCCCTTGAATGCCCTGCTGGTACTGTACTCAGCGATGGAACACATCTACTATAA 1190
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Db 356 ATGTTTAAACAGGATGCCCTGCTGGTACAGTGGTTGATGATGATGACATCACTAATTTGT 297
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1191 ATAAGCAGCATCTGAATGTTTAAATGCTGCCCACTTTTATATACTACAAATAAACTGA 1250
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Db 296 AGCTTTAGCAAGTGAATGTACTAAATGTTAGCTAACTTTTATGCATCAAAACATCTGG 237
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QY 1251 TTGGGTAGCAGGTATGATACATGTACTAGTTGTAATAAATAAATAAATTAATCTGCGCTGA 1310
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Db 236 TTTTGCAGCAGGTACTGATACATGTACTGAAATGTTCTAAAATAATTAATCTTCTGGTGCTAC 177
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1311 AGCTAATTTACCTGAATCTGCTAAAAAAATAATAATGTG-----ATTTCGCTAA 1361
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Db 176 AGCTAAGTATATGCTGAAGCTACTTAAAAAGCATAATGCGCAGTTTCCACTTTTCGCAA 117
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1362 TTTTATCAATTCCTCTAATTAATGATTTCTTATTAATTAT 1403
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 116 ATTTTATCAATGCTCTAATAATTTATTTCTTTCTATTGTT 75
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RESULT 5
BQ134889/c 502 bp mRNA linear EST 22-APR-2002
LOCUS INIT1_1_D07.b1_A006 G5 trophont cDNA (INIT1) Ichthyophthirius
DEFINITION multifiliis cDNA, mRNA sequence.
ACCESSION BQ134889
VERSION BQ134889.1 GI:20260988
KEYWORDS EST.
SOURCE Ichthyophthirius multifiliis.
ORGANISM Ichthyophthirius multifiliis
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Ophryoglenina; Ichthyophthirius.
REFERENCE 1. (bases 1 to 502)
AUTHORS Clark,T., Cordonnier-Pratt,M.-M., Sudman,M., Wentzel,V., Gingle,A.,
Dickerson,H., Lin,T.-L. and Pratt,L.H.
TITLE An EST database for Ichthyophthirius multifiliis (G5 isolate)
JOURNAL Unpublished (2002)
COMMENT Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector, and regions
below Phred quality 16. The threshold for highest quality sequence
is 20.
Seq primer: JEN REV
High quality sequence stop: 474
POLYA=Yes.

FEATURES
source Location/Qualifiers
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/organism="Ichthyophthirius multifiliis"
/db_xref="G5"
/db_xref="taxon:5932"
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/clone_lib="G5 trophont cDNA (INIT1)"
/notes="Vector: pBluescript SR(-) from Lambda Zap II;
Site_1: EcoRI; Site_2: EcoRI; The library was made from
trophont polyA+ RNA of the G5 parasite strain.
Double-stranded cDNA was linked to EcoRI adaptors, size
fractionated, and material >500 bp cloned into lambda Zap
II. Plasmid DNA for sequencing was prepared by mass
excision."
BASE COUNT 185 a 80 c 70 g 167 t
ORIGIN
Query Match 11.8%; Score 165.6; DB 14; Length 502;
Best Local Similarity 67.2%; Pred. No. 7.5e-46;
Matches 285; Conservative 0; Mismatches 124; Indels 15; Gaps 3;
QY 989 CAGATGTCTAAATGTGCTGCTAACTTTTATTTTGTGTTGTAATAATTTCTAGCGAGGAA 1048
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Db 498 CATAATGTTTAAATGTTAAAGCTGGCTTTTACT---AAATAGTAATTTTGAAGCAGGTA 442
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QY 1049 GTAGTAGATGCAAGCATGTCCAGCAATAAAGTTTAAAGCGCTGTAGCAACTGCAGGTG 1108
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Db 441 AAAGTTAATGCAATAAGTGTGCAGTAGTAAACT---GGTTACAGCATCTGTTCCAGGTA 385
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1109 GTACTGCTACTTTAATTCGTAATGTGCCCTTGAATGCCCTGCTGCTGCTACTGCTACCG 1168
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 384 ATAGTGCTACTTCAGCCACATAATGTTTAAACGATGTGCCCTGCTGGTACAGTGGTTGATG 325
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1169 ATGGAACAACATCTACTTATAATAAAGCAGCATCTGTAATGTGTTAAATGTGTCGCCAAT 1228
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 324 AUGGTACATCACTAATTTGTAGCTTTAGCAAGTGAATGTAATAATGTTAGGCTAACT 265
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QY 1229 TTTTACTACAAAAATAACTGATTCGGGTAGCAGGTATTTGATGATACATGCTAGTTGTAATA 1288
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Db 264 TTTATGCATCAAAAAACATCTGTTTTCAGCAGGCTACTGATACATGCTGAATGTTCTA 205
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1289 ARAAATTAATCTCTGCGCTGAAGCTAATTTACCTGAATCTGCTAAAAAATAATAAT 1348
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Db 204 ARAAATTAATCTCTGCTGCTACAGCTAAAGTATATGCTGAAGCTACTTAAAAAGCATAAT 145
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1349 GTG-----ATTTCGCTAATTTTATCAATTTCTTATTTATTTATTTATTTATTT 1399
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 144 GCGCCAGTTCCACTTTTCGCAAAATTTTATCAATGCTCTTAATATTTATTTCTTCTATT 85
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1400 TATT 1403
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Db 84 TGT 81

RESULT 6
BQ134871/c 445 bp mRNA linear EST 22-APR-2002
LOCUS INIT1_B05.b1_A006 G5 trophont cDNA (INIT1) Ichthyophthirius
DEFINITION multifiliis cDNA, mRNA sequence.
ACCESSION BQ134871
VERSION BQ134871.1 GI:20260970
KEYWORDS EST.
SOURCE Ichthyophthirius multifiliis.
ORGANISM Ichthyophthirius multifiliis
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Ophryoglenina; Ichthyophthirius.
REFERENCE 1. (bases 1 to 445)
AUTHORS Clark,T., Cordonnier-Pratt,M.-M., Sudman,M., Wentzel,V., Gingle,A.,
Dickerson,H., Lin,T.-L. and Pratt,L.H.
TITLE An EST database for Ichthyophthirius multifiliis (G5 isolate)
JOURNAL Unpublished (2002)
COMMENT Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector, and regions
```

---:--- ---, Sadman, M., Wentzel, V., Vingle,

QT35130.1 GI:20261293

NOTES

BQ135196
INT1_E06.g1_A006 G5 trophont cDNA (INT1) Ichthyophthirius
multifiliis cDNA, mRNA sequence.
BQ135196
BQ135196
BQ135196.1 GI:20261295

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KEYWORDS EST.
SOURCE Ichthyophthirius multifiliis.
ORGANISM Ichthyophthirius multifiliis
REFERENCE Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
AUTHORS Hymenostomatida; Ophryoglenina; Ichthyophthirius.
TITLE 1 (bases 1 to 675)
JOURNAL Clark,T., Cordonnier-Pratt,M.-M., Sudman,M., Wentzel,V., Gingle,A.,
COMMENT An EST database for Ichthyophthirius multifiliis (G5 isolate)
unpublished (2002)
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector, and regions
below Phred quality 16. The threshold for highest quality sequence
is 20.
Seq primer: T7
High quality sequence start: 42
High quality sequence stop: 675
POLYA-No. Location/Qualifiers
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/organism="Ichthyophthirius multifiliis"
/strain="G5"
/db_xref="taxon:5932"
/clone_lib="G5 trophont cDNA (INIT1)"
/note="Vector: pBluescript SK(-) from Lambda Zap II;
Site_1: EcoRI; Site_2: EcoRI; The library was made from
trophont polyA+ RNA of the G5 parasite strain.
Double-stranded cDNA was linked to EcoRI adaptors, size
fractionated, and material >500 bp cloned into lambda Zap
II. Plasmid DNA for sequencing was prepared by mass
excision."
BASE COUNT 216 a 126 c 127 g 206 t
ORIGIN
Query Match 9.6%; Score 134.4; DB 14; Length 675;
Best Local Similarity 63.3%; Pred. No. 4.6e-19;
Matches 291; Conservative 0; Mismatches 156; Indels 13; Gaps 5;
Qy 819 TCCTAATTTTCAATCCAGGTAATAGTACATGCGCTTACCTGCCAGCAATAAAGATTATGG 878
Db 459 TCCTATGGTTCCTGGCCCTAATAGTAAATGCGTAGCTTCGGAATCAAAAAGACCAA--- 403
Qy 879 TGCTGAAGCCACTGCAGGTGGTCCGCTACTTTAGCCAAATAATGTAATATTGATGCCC 938
Db 402 TTCTAATCCAGATCAGTCTTGAGGCTAATTTAGCGCATATATGGCACTGAATGTCC 343
Qy 939 TGATGGTACTGCAATTCGTAGTGAG---CAACTAATTTATGTAATATTATAAACAAGATG 995
Db 342 TGCTGGCACTTGTGACAGCGAGTAACACCTACTTATACGTATCACTCTCATATAG 283
Qy 996 TCTAATTTGCTGCTAACTTTTATTTTATGTTATGTTATTTAGCGAGGAAGTAGTAG 1055
Db 282 TGTTAATTTGTAAGCTGCCTTTTACT---AAATAGTAATTTTGAAGCAGGTAAGATTA 226
Qy 1056 ATGCAAGCATGTCAGCAATAAAGTTTAAAGGCGTGTAGCAACTGCAGGTGGTACTGC 1115
Db 225 ATGCAATAAGTGTGCAGTAAGTAAACT---GGTTCAGCATCTGTCCAGGTAAATAGTGC 169
Qy 1116 TACTTTAATTCGTAATGTGCCCTTGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1175
Db 168 TACTTCAGCCACATAATGTTTAAACGATGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 109
Qy 1176 AACATCTACTTTATAAATAAGCAGCATCTGAATGTGTTAAATGTGCTGCCAATTTTATAC 1235
Db 108 ATCAACTAATTTGTAGCTTTTGAAGCAAGTGAATGTACTAAATGTAGGCTAACTTTTATGC 49
Qy 1236 TACAAAATAAATGATTGGGTAG-CAGGTATTGATACATG 1274

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Db 48 ATCAAAAACATCTGGTTTGCAGCCAGGTACTGATACACG 9
RESULT 9
BQ134821/c 599 bp mRNA linear EST 22-APR-2002
LOCUS INIT1.4_D09.bl_A006 G5 trophont cDNA (INIT1) Ichthyophthirius
DEFINITION multifiliis cDNA, mRNA sequence.
ACCESSION BQ134821
VERSION BQ134821.1 GI:20260920
KEYWORDS EST.
SOURCE Ichthyophthirius multifiliis.
ORGANISM Ichthyophthirius multifiliis
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Ophryoglenina; Ichthyophthirius.
REFERENCE 1 (bases 1 to 599)
AUTHORS Clark,T., Cordonnier-Pratt,M.-M., Sudman,M., Wentzel,V., Gingle,A.,
Dickerson,H., Lin,T.-L. and Pratt,L.H.
TITLE An EST database for Ichthyophthirius multifiliis (G5 isolate)
JOURNAL Unpublished (2002)
COMMENT Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector, and regions
below Phred quality 16. The threshold for highest quality sequence
is 20.
Seq primer: JEN REV
High quality sequence stop: 506
POLYA-No. Location/Qualifiers
1..599
/organism="Ichthyophthirius multifiliis"
/strain="G5"
/db_xref="taxon:5932"
/clone_lib="G5 trophont cDNA (INIT1)"
/note="Vector: pBluescript SK(-) from Lambda Zap II;
Site_1: EcoRI; Site_2: EcoRI; The library was made from
trophont polyA+ RNA of the G5 parasite strain.
Double-stranded cDNA was linked to EcoRI adaptors, size
fractionated, and material >500 bp cloned into lambda Zap
II. Plasmid DNA for sequencing was prepared by mass
excision."
BASE COUNT 191 a 113 c 111 g 183 t 1 others
ORIGIN
Query Match 9.1%; Score 127.8; DB 14; Length 599;
Best Local Similarity 62.8%; Pred. No. 1.2e-17;
Matches 269; Conservative 0; Mismatches 147; Indels 12; Gaps 4;
Qy 819 TCCTAATTTTCAATCCAGGTAATAGTACATGCGCTTACCTGCCAGCAATAAAGATTATGG 878
Db 431 TCCTATGGTTCCTGGCCCTAATAGTAAATGCGTAGCTTCGGAATCAAAAAGACCAA--- 375
Qy 879 TGCTGAAGCCACTGCAGGTGGTCCGCTACTTTAGCCAAATAATGTAATATTGTCATGCC 938
Db 374 TTCTTAATCCAGATCAGGTCTTGGAGCTAATTTAGCCGCAATAATGTCGCACTGAATGCC 315
Qy 939 TGATGGTACTGCAATTCGTAGTGAG---CAACTAATTTATGTAATATTATAAACAAGATG 995
Db 314 TGCTGGCACTTTGTTACAGACGAGTAACACCTACTTATCTATCTATCTCTCATAATG 255
Qy 996 TCTAATTTGCTGCTAACTTTTATTTTATGTTAGTAAATTTCTAGCAGGAAGTAGTAG 1055
Db 254 TGTTAATTTGTAAGCTGCCTTTTACT---AAAATAGTAATTTTCAAGCAGGTAAGATTA 198
Qy 1056 ATGCAAGCATGTCAGCAATAAAGTTTAAAGGCGCTGTAGCAACTGCAGGTGGTACTGC 1115
Db 197 ATGCAATAAGTGTGCGAGTAAGTAAACT---GGTTCAGCATCTGTTCCAGGTAAATAGTC 141

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Db	153	ATAAATACTGTGACTCATTTGCTAAAAACACACTTTTACTTTAATGGTGGTAATCCCTGCAGGT	212
QY	175	-----TTCCGTTCTCGTGTAGTGTACACCTTTGTCCATAA	213
Db	213	CAGGCTCCTGGTGTACAAATTCAGTCCAGTGTTTACGTGCATAGTGTGCCAAGTA	272
QY	214	AAAAAGATGCTGGTGTCTTAACCAAAATCCACCTGCTACTGCTAAATTTAGTCACATAATGT	273
Db	273	CACAAA---GCCGATCTCAACACAGATAAGCTGGTGTATGCTAAATTTAGCCGCAATAATGT	329
QY	274	AACGTTAAATGCCCTGCTGGTACGCCAAATCCAGCTGGAGCAACAGATTAATGCAGCAATA	333
Db	330	AGCAACTATATGCTGCTGGCAGCTCCAGTTCAAAGATGGATCCACTCTTTTACTTAATCC	389
QY	334	ATCACAGAAATGTTTAATGTAGAAATTAATTTTATATGAANAATGT	381
Db	390	CTCACATAATGTGTTAATGTGAACCTAACTTTTACTTTAATGGTGT	437
RESULT 11			
LOCUS	BQ134810		
DEFINITION	BQ134810 538 bp mRNA linear EST 22-APR-2002		
ACCESSION	INT11.4_C08.bl_A006 G5 trophont cDNA (INIT1) Ichthyophthirius		
VERSION	BQ134810		
KEYWORDS	BQ134810.1 GI:20260909		
SOURCE	EST.		
ORGANISM	Ichthyophthirius multifiliis.		
REFERENCE	Ichthyophthirius multifiliis.		
AUTHORS	Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Ophryoglenia; Ichthyophthirius.		
TITLE	1 (bases 1 to 538)		
JOURNAL	Clark, T., Cordonnier-Pratt, M.-M., Sudman, M., Wentzel, V., Gingle, A.,		
COMMENT	Dickerson, H., Lin, T.-L., and Pratt, L.H.		
	An EST database for Ichthyophthirius multifiliis (G5 isolate)		
	Unpublished (2002)		
	Contact: Cordonnier-Pratt MM		
	Laboratory for Genomics and Bioinformatics		
	The University of Georgia, Department of Plant Biology		
	Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA		
	Tel: 706 542 1860		
	Fax: 706 583 0210		

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POLYA=NO.
Location/Qualifiers
1..538
/organism="Ichthyophthirius multifiliis"
/strain="G5"
/db_xref="taxon:5932"
/clone_lib="G5 trophont cDNA (INTrl)"
/note="Vector: pBluescript SK(-) from Lambda Zap II; Site_1: EcoRI; Site_2: EcoRI; The library was made from trophont polyA+ RNA of the G5 parasite strain. Double-stranded cDNA was linked to EcoRI adaptors, size fractionated, and material >500 bp cloned into lambda ZAP II. Plasmid DNA for sequencing was prepared by mass excision."
155 a      101 c      106 g      175 t      1 others
BASE COUNT
ORIGIN
Query Match          8.1%; Score 113.8; DB 14; Length 538;
Best Local Similarity 59.2%; Pred. No. 1.4e-14;
Matches 234; Conservative 0; Mismatches 152; Indels 9; Gaps 2;

QY    171 TCGTTTCGTCTCGTGTAGTGTAACCTTGTCATAAAAAGAATGCTGGTGC 230

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QY	231	TTAACCAATCCACTGCTACTGCTAATTTAGTCACATAATGTAACGTTAAATGCCCTGC	290
Db	209	TTAATCCAGATCAGGCTTGGAGCTAATTAGCCGATAAATGGTCACCTGAATGTCCTGC	268
QY	291	TGGTACCCGAATTCAGGTGGAGCAACA--GATTATGCAGCAATAATCACAGAAATGTG	347
Db	269	TGGCACTCTTGTACAGACGGAGTAACACCTACTTTAATCTGTATCACCTCTCATATGTG	328
QY	348	TAATGTGAGAATTAATTTTATATGAATGCTCCAAATTTTAATGCAGGTGCTAGTAC	407
Db	329	TAATTTGAAGTGCGCTTTACTAAAATAGT-----AATTTCGAAGCAGGTAAGAAGTTA	382
QY	408	ATGCACAGCTTCTCCGGTAAACAGAGTTGTTGTTGCTGACTGCTGTTAATCGCGCTAC	467
Db	383	ATGCAATAAGTGTGCAGTAAGTAAAACTGGTTCAGCATCTGTTCCAGGTAATATAGTGCTAC	442
QY	468	CATAGTCGCATAATGTACGTCGCATGTCCTACTGCTACTGCACCTTGATGATGGAGTAAC	527
Db	443	TTCCAGCACATAATGTTAAAAACGATTCGCCCTGCTGGTACAGTGGTTGATGATGGTACATC	502
QY	528	TACTGATTATGTAGATCATTTACAGAGAAATGTGTTA	562
	503	ANCTAATTTTGTAGCTTTAGCAAGTGAATGACTA	537

RESULT 12		mRNA linear EST 22-APR-2002
BQ134905	630 bp	
LOCUS	trophont cDNA (INIT1)	Ichthyophthirius
DEFINITION	multiple cDNA, mRNA sequence.	

ACCESSION	BQ134905
VERSION	BQ134905.1
KEYWORDS	GI:20261004
SOURCE	EST
ORGANISM	Ichthyophthirius multifiliis.
REFERENCE	Ichthyophthirius multifiliis. Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Ophryoglenina; Ichthyophthirius.
AUTHORS	1 (bases 1 to 630) Clark, T., Cordonnier-Pratt, M.-M., Sudman, M., Wentzel, V., Gingle, A., Dickerson, H., Lin, T.-L. and Pratt, L.H.
TITLE	An EST database for Ichthyophthirius multifiliis (G5 isolate)
JOURNAL	Unpublished (2002)
COMMENT	Contact: Cordonnier-Pratt MM Laboratory for Genomics and Bioinformatics The University of Georgia, Department of Plant Biology Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA Tel: 706 542 1860 Fax: 706 583 0210 Email: mmpratt@uga.edu Sequences have been trimmed to exclude PolyA, vector, and regions below Phred quality 16. The threshold for highest quality sequence is 20. Seq primer: JEN REV High quality sequence stop: 629 POLYA=No.

FEATURES	Location/Qualifiers
source	1..630
	/organism="Ichthyophthirius multifiliis"
	/strain="G5"
	/db_xref="taxon:5932"
	/clone_lib="G5 trophont cDNA (INIT1)"
	/note="Vector: pBluescript SK(-) from Lambda Zap II; Site_1: EcoRI; Site_2: EcoRI; The library was made from trophont polyA+ RNA of the G5 parasite strain. Double-stranded cDNA was linked to EcoRI adaptors, size fractionated, and material >500 bp cloned into lambda Zap II. Plasmid DNA for sequencing was prepared by mass excision."

BASE COUNT	179 a	120 c	118 g	213 t
ORIGIN				
Query Match		7.9%	Score 110.4;	DB 14; Length 630;

[illegible]

342 ATGTGTTAATTGTAGAAATTAAATTTTATATATGAAATGCT 381
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371 ATGTGTTAATTGTAAACCACTTTTACTTTAATGGTGGT 410
|||||

RESULT	13
BQ134827	
LOCUS	mRNA linear EST 22-APR-2002
DEFINITION	BQ134827 631 bp trophont cDNA (INIT1) Ichthyophthirius multifiliis cDNA. mRNA sequence.

ACCESSION	BQ134827
VERSION	BQ134827.1
KEYWORDS	GI:20260926
SOURCE	EST.
ORGANISM	<i>Ichthyophthirius multifiliis</i> .
	<i>Ichthyophthirius multifiliis</i>
	Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
	Tetrahymena; Tricostema; Ichthyophthirius.

REFERENCE	1 (bases 1 to 631)
AUTHORS	Clark, T., Cordonnier-Pratt, M.-M., Sudman, M., Wentzel, V., Gingle, A., Dickerson, H., Lin, T.-L. and Pratt, L.H.
TITLE	An EST database for <i>Ichthyophthirius multifiliis</i> (G5 isolate)
JOURNAL	Unpublished (2002)
COMMENT	Contact: Cordonnier-Pratt MM Laboratory for Genomics and Bioinformatics The University of Georgia, Department of Plant Biology Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA Tel: 706 542 1860 Fax: 706 583 0210 Email: mmpratt@uga.edu Sequences have been trimmed to exclude polyA, vector, and regions below phred quality 16. The threshold for highest quality sequence is 20.

Seq primer: JEN REV
High quality sequence stop: 630
polYA=No.

FEATURES	Location/Qualifiers
1..631	
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	/strain="G5"
	/db_xref="taxon:5932"
	/clone_lib="G5 trophont cDNA (INIT1)"
	/note="Vector: pBluescript SK(-) from Lambda Zap II; Site_1: EcoRI; Site_2: EcoRI: The library was made from trophont polyA+ RNA of the G5 parasite strain. Double-stranded cDNA was linked to EcoRI adaptors, size fractionated, and material >500 bp cloned into lambda Zap II."

Laboratory for Genomics and Bioinformatics
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Tel: 706 542 1860
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Sequences have been trimmed to exclude PolyA, vector, and regions below Phred quality 16. The threshold for highest quality sequence is 20.

Seq primer: JEN REV
High quality sequence stop: 502

Thu Feb 20 11:10:20 2003

us-09-497-967-3.rst

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FEATURES
source
POLYA=No.
Location/Qualifiers
1..514
/organism="Ichthyophthirius multifiliis"
/strain="G5"
/db_xref="taxon:5932"
/clone_lib="G5 trophont cDNA (IN11)"
/note="Vector: pBluescript SK(-) from Lambda Zap II;
Site 1: EcoRI; Site 2: EcoRI; The library was made from
trophont polyA+ RNA of the G5 parasite strain.
Double-stranded cDNA was linked to EcoRI adaptors, size
fractionated, and material >500 bp cloned into lambda ZAP
II. Plasmid DNA for sequencing was prepared by mass
excision."
BASE COUNT 166 a 96 c 102 g 149 t 1 others
ORIGIN
Query Match 7.6%; Score 106.4; DB 14; Length 514;
Best Local Similarity 60.8%; Pred. No. 5.6e-13;
Matches 192; Conservative 0; Mismatches 121; Indels 3; Gaps 1;
QY 366 TTATAATGAATACTCTCAAAATTTAATGCGAGGTGCTAGTACATGCACAGCTTGTCGGGT 425
Db 431 TAATAATCCTGAAGTTCCTAATGTTCTAGCCCTAATGGTTAATGGTAGCTTGCTAAGT 372
QY 426 AAACAGAGTTGGTGGTGCATTGACTGCTGTAATGCCGCTACCAATAGTCGCATATGTAA 485
Db 371 AAACAAGTCTGATTCCTCAATTAAGACCAGGTGCTTAGGCTTAATTTAGCCACATAATGTAA 312
QY 486 CGTCGCATGCTCTACTGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 545
Db 311 CAATGAATGCTCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 252
QY 546 ATTCACAGATGCTGTAAATAGACTTAATCTTACTATATGCTTAATGCTTAATAC 605
Db 251 AATCTCATATGTAATCTTTTCTAAAGTGAATTTTACTTTTAAATGGTGGCAA--TCCTTC 195
QY 606 TCCTTTCAATCCAGTAAAGTTAATGCACACCTTGTCGGCAATTAACCTGCTAATGT 665
Db 194 AGCTCAGAAATCCTGGTAATGATTAATTCACCTCCAGGTTAATGATTCGAATCCTGATGC 135
QY 666 TGCTTAAGCTACTTTA 681
Db 134 TGCTACTGCTGCTTAA 119
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